RNA or a DNA that competes with an mRNA for a gene that has been confirmed to be influenced by the endocrine disruptor is prepared. A competitive RT-PCR is conducted using the RNA or the DNA as an internal standard. The expression level of the influenced gene is then quantitatively determined by the competitive RT-PCR.

As described above, the presence or the absence of an endocrine disruptor can be substantially and readily judged using the expression of a gene that is influenced by a endocrine disruptor (for example, a gene for a nuclear receptor in a cell or one of a number of downstream genes) as an index according to the method of the present invention.

(3) A substance that potentially causes endocrine disruption can be detected as follows.

As used herein, a substance that potentially causes endocrine disruption means a substance that potentially influences the normal activity of a hormone which is naturally exerted in a living body. Substances of which the activities have been already confirmed and substances of which the activities have not been confirmed yet are included within the definition.

A DNA array for detecting a substance that potentially causes endocrine disruption is prepared by immobilizing in a manner as described above a gene which

has been confirmed to be influenced by an endocrine disruptor according to a method as described in (1) above.

A nucleic acid sample is prepared from a cell, a tissue or an organism which has been exposed to a sample that is suspected to contain a substance that potentially causes endocrine disruption as described above. The nucleic acid sample is then hybridized as described above. Change in gene expression can be determined based on the difference between the signal intensities. The substance can be judged as an endocrine disruptor based on the results.

A substance can be considered to be an endocrine disruptor based on the results not only in case where changes in signals are observed for all of the DNAs on the DNA array but also in case where the changes are observed for a portion of the DNAs. In particular, if the changes in signal strength are observed for a portion of the DNAs, the detection method can be optimized by further selecting the genes that are influenced by the substance action according to the method as described in (1) above such that a substance that causes endocrine disruption as the substance does can be detected more exactly.

In another embodiment, an RNA or a DNA that competes with an mRNA for a gene that has been confirmed to be influenced by the endocrine disruptor as described above

is prepared. A competitive RT-PCR is conducted using the RNA or the DNA as an internal standard. The degree of endocrine disruption can be quantitatively detected based on the expression of the gene. Any methods can be preferably used for detecting, or quantifying the expression of, a gene that is influenced by an endocrine disruptor obtained as described in (1) above as long as the methods can be used for the detection/quantification of the gene.

(4) The DNA array of the present invention

As used herein, a DNA array refers to a support onto which a gene or a fragment thereof is immobilized and includes, for example, a so-called DNA chip.

Any supports which can be used for hybridization may be used for the DNA array of the present invention. Usually, a slide glass, a silicone chip, a nitrocellulose or nylon membrane or the like is used. Preferably, a support made from a material which is non-porous and has a smooth surface (e.g., a glass such as a slide glass) can be preferably used. Any supports having surfaces onto which DNAs can be immobilized through covalent bonds or non-covalent bonds can be used. Supports having hydrophilic or hydrophobic functional groups on their surfaces are preferably used. Examples of the preferable functional groups on the surfaces of the supports include, but are not